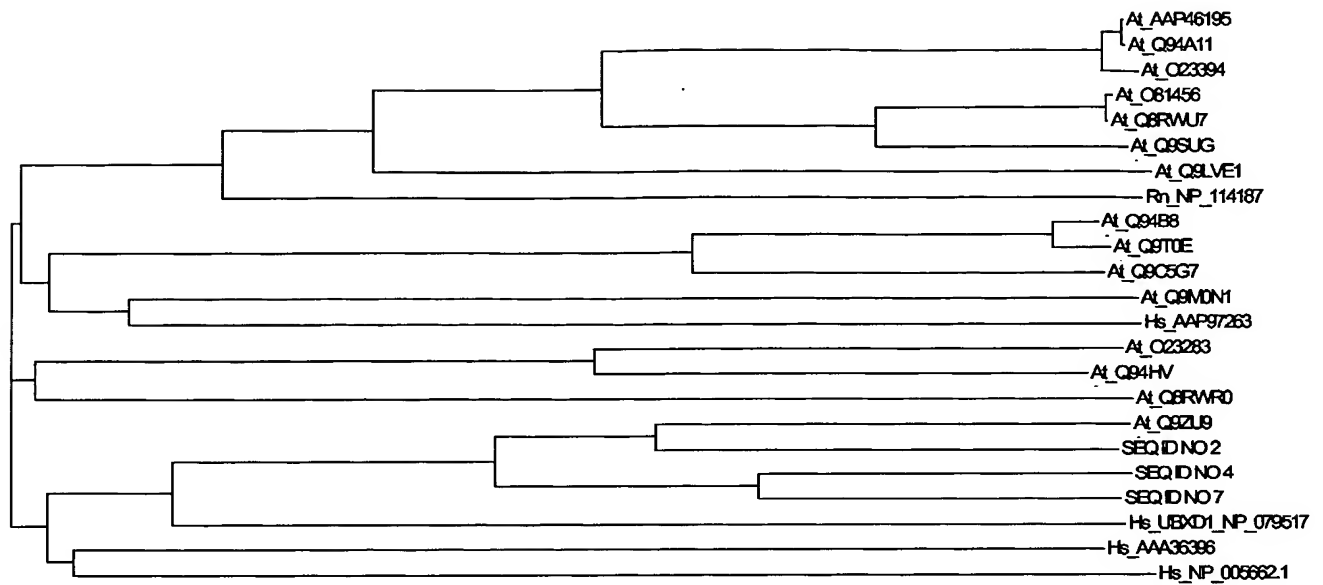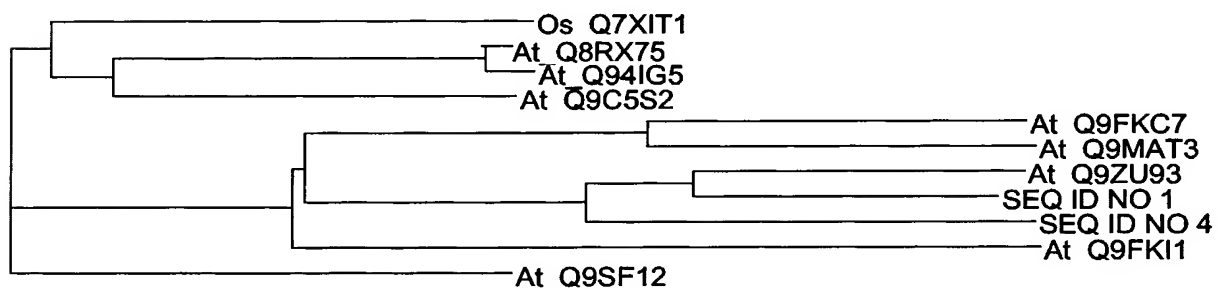**FIGURE 1 A**

FIGURE 1B

```
Consensus terms for the UBX domain
YJE8_YEAST       KGFLAQ-NYCTLQLKLPNGYTISNTFP-PQTKLHKVRMWL----DYNCYDDGTP-----
CONSENSUS/80%    s.t..t...splplRhssGpph.ppF..spp.lptlhthl........s.sss.......
CONSENSUS/65%    stpptt.stsplQlRhssGpphsppFs.uppslpplhphl....t...s.ssss......
CONSENSUS/50%    Ppppss.sps+LQlRhPDGpplsccFs.us-sLcplapaV....sptpssusss......

YJE8_YEAST       --------YLFHRNIPRVTLTRNDELKSLQEL-DLLPRSTLILEP
CONSENSUS/80%    ........apl.pshPch.hspt-..hph.p..thhspsslll..
CONSENSUS/65%    ........FpL.pshP+c.hsps-..ppl.ch.tlhPsusllllt.
CONSENSUS/50%    ........FpLpssaPR+slocsD..KoLp-l.sLhPsuoLlLct


Consensus terms for the PUG domain
AAF74723         EASKLLLTYADNILRNPSDEKYRSIRIGNTAFSTRLLPVRGAVECLFEMGFEEG-----
CONSENSUS/80%    tslt.LLphhcNhhpp.p-.........s..hpphlh.h.tsh..h...tF.ph......
CONSENSUS/65%    pslpsLL+hl+Nhhcc.pE.........stthpctltpl.sshphhhthtFscl.h....
CONSENSUS/50%    solccLLRhlRNlh+HhcEt.......tsppl+EplGslP-uhcpaFsssFPcLhh....

AAF74723         --ETHLIFPK
CONSENSUS/80%    ...phh.h.p
CONSENSUS/65%    ...phathhp
CONSENSUS/50%    ...csYplss
```

FIGURE 2 A

UBX domain present in SEQ ID NO 2

339 KAARKKYTKSIIRVQFPDGALLQGVFLPSEPTSALYEFVSAALKEPSLEFELLHPVLVKKRVIPHF
PAAGERAVTVEEEDLVPAALLKFK 428

PUG domain present in SEQ ID NO 2:

173 GSVEVVIKLLKNIVKEPENAKFRKIRMGNPKIKGAIGDVVGGVELLEFVGFELKEEGGEIWAVMDV
PS 240

UBX domain present in Q9ZU93

345 KAARKRYKRSMIRVQFPDGVVLQGVFAPWEPTFALYEFVSSALKEPSLQFELLDPVLVKRRVIPHT
PAPGQKPITLEDEELVPSALIRFRP 435

PUG domain present in Q9ZU93

181 SSIDVLLRLFKNIVKEPENAKFRKVRMSNAKIKEAIGDVAGGVELLELVGFELKEENDEIWAVMDV
PS 248

FIGURE 2 B

```
Q9ZU93         1 MDDVKDKLKGFMKKVNLSSSSGKFKGQGRVLGSSSSSSAPPVNPIQNRFN      50
                 |.|:|||:||||||||. ||||||||||||||||||.|||.  |.|.: |.|:
SEQ_ID_NO_2    1 MGDMKDKVKGFMKKVT-SSSSGKFKGQGRVLGGSSSSG--PSNHV-NNFS      46

Q9ZU93        51 S-------SQAPNPTPRPKPNPNPLPEKPLSSSDQKISGSTR---NPDHD      90
                 |        .|.|:.|         ...|:|| |:|||:|.....    |....
SEQ_ID_NO_2   47 SHPLNTRQDQQPSYT-------KTSPQKP-SNSDQRIENICEIQFNKSES   88

Q9ZU93        91 PVRAPQDGFDPYGAFITSSNRSQNGYSL-SMFECPICKNPFTSEEEVSVH     139
                   :|||||:|..:||..|:..|||| ::|||||:|.:.|.||||||.|
SEQ_ID_NO_2   89 -----KDGFDPFGELVTSGKRNPKGYSLTNVFECPVCGSGFVSEEEVSTH     133

Q9ZU93       140 VESCLG---DTN-GDESSFEKDNNDNDKSEMEKLVVVYLSGKPSESSIDV     185
                 ::|||.    .:|  |.||..|.        |||:|..|..|:||||||.|::|
SEQ_ID_NO_2  134 IDSCLSSEVSSNLGVESKVEV------KSELETCVSAYVSGKPSEGSVEV     177

Q9ZU93       186 LLRLFKNIVKEPENAKFRKVRMSNAKIKEAIGDVAGGVELLELVGFELKE     235
                 ::::|.||||||||||||||||:||.|.|||.|||||.||||||.||||||
SEQ_ID_NO_2  178 VIKLLKNIVKEPENAKFRKIRMGNPKIKGAIGDVVGGVELLEFVGFELKE     227

Q9ZU93       236 ENDEIWAVMDVPSEEQSILINKVVGYLEKRKTESSGSSAQV--MEPVAPK     283
                 |..||||||||||||.:::..||..||.:|.|...|.:||  .|||.||
SEQ_ID_NO_2  228 EGGEIWAVMDVPSEEQLVMLKNVVSLLEPKKVEELASLSQVKASEPVEPK     277

Q9ZU93       284 KIDREIRVFFSVSENVASRIEVPDSFYSLSADEIKREADLRRKKIAESQL     333
                 ||||:|||||||.|:||::||:|||||::||.:|::|||::|:||:.:|:|
SEQ_ID_NO_2  278 KIDRQIRVFFSVPESVAAKIELPDSFFNLSREELRREAEMRKKKLEDSKL     327

Q9ZU93       334 LIPRSYKEKQAKAARKRYKRSMIRVQFPDGVVLQGVFAPWEPTFALYEFV     383
                 |||:||:||||||||||||||:|.:|:||||||||.:|||||.|.|||.||||||
SEQ_ID_NO_2  328 LIPKSYREKQAKAARKKYTKSIIRVQFPDGALLQGVFLPSEPTSALYEFV     377

Q9ZU93       384 SSALKEPSLQFELLDPVLVKRRVIPHTPAPGQKPITLEDEELVPSALIRF     433
                 |:|||||||:||||.|||||:|||||.||.|::.:|:|:|:|||:||::|
SEQ_ID_NO_2  378 SAALKEPSLEFELLHPVLVKKRVIPHFPAAGERAVTVEEEDLVPAALLKF     427

Q9ZU93       434 RPIETDSLVFTGLRNELLEISEPLS          458
                 :||||||:|||||.|||||||||.
SEQ_ID_NO_2  428 KPIETDSVVFTGLCNELLEISEPLETGSVASS  459
```

FIGURE 2 C

4/9

```
SEQ_ID_NO2      1 MGDMKDKVKGFMKKVTSSSSG---KFKGQGRVLGGSSSSGPSNHVNNFSS      47
                  .||||:|.|||||||.||   .|||...|||     ||||..    ||
SEQ_ID_NO4_C    1 mmkdkmkefmkkvtssgsgtpssfkgtshvlg----sgpsps----ss      40

SEQ_ID_NO2     48 HPL----NTRQDQQPSYTKTSPQKPSNSDQRIENICEIQFNKSESKDGFD      93
                  ||.    |...:.:|:..:|||..|........:.:
SEQ_ID_NO4_C   41 hpaarssnpspnlrpapkrtspptpptlttdlts---------------      74

SEQ_ID_NO2     94 PFGELVTSGKRNPKGYS---LTNVFECPVCGSGFVSEEEVSTHIDSCLSS     140
                  |..||....|.|....      ......||.||..|.||..||.|:|.||:|
SEQ_ID_NO4_C   75 -ftplvcyssrrpdangtaCavatvacpscgdafpselavsehldgclas     123

SEQ_ID_NO2    141 EVSSNLGVESKVEVKSELETCVSAYVSG--KPSEGSVEVVIKLLKNIVKE     188
                  ..     |..::           .:||:..  .|...|||||.:||.|:::|
SEQ_ID_NO4_C  124 ag----garar---------aaaylaadppppaasvevvkrllgnllre     159

SEQ_ID_NO2    189 PENAKFRKIRMGNPKIKGAIGDVVGGVELLEFVGFELKEEGGEIWAVMD-     237
                  |.|.|||::|:|||:||.|:..|..||||||||.|||.::|||||.:||||
SEQ_ID_NO4_C  160 pgndkfrrvrlgnprikealadrdggvelleavgftvgdeggepfavmde     209

SEQ_ID_NO2    238 VPSEEQLVMLKNVVSLLE-------PKKVEELASLSQVKASEPVE-PKKI     279
                  |||:..|..::..|.|||       |.|.|..|..|....|:..| .|.|
SEQ_ID_NO4_C  210 vpsdprlngirravllllegahpsappvkaeaeakescsnvsdvqegakti     259

SEQ_ID_NO2    280 DRQIRVFFSVPESVAAKIELPDSFFNLSREELRREAEMRKKKLEDSKLLI     329
                  |||||||.|||.|..|:..:|||:.||.||.||:|.||:||:::||.|:|||
SEQ_ID_NO4_C  260 drqirvfvsvpgssmaqndvpdsfyklsgeeirneakmrrerleqsrlli     309

SEQ_ID_NO2    330 PKSYREKQAKAARKKYTKSIIRVQFPDGALLQGVFLPSEPTSALYEFVSA     379
                  ||||:||||.|||:||.:::|||||||..:|||:|||.|.|.||:||||::
SEQ_ID_NO4_C  310 pksykekqalaarqkykqavirvqfpdrmilqgiflpgeatsslyefvts     359

SEQ_ID_NO2    380 ALKEPSLEFELLHPVLVKKRVIPHFPAAGERAVTVEEEDLVPAALLKFKP     429
                  |||:..|||||:.|.::.|.||:||||..||||.|::||:|||:|||||.|
SEQ_ID_NO4_C  360 alkqsglefelispaipkprvvphfpnpgerartlqeeelvpsallkfip     409

SEQ_ID_NO2    430 IETDSVVFTGLCNELLEISEPLETGSVASS           459
                  .||||:|||||.:|||..||||...|.
SEQ_ID_NO4_C  410 ketdsmvftglldellmaseplpaasq             436
```

FIGURE 2 D

```
SEQ_ID_NO_4    1 mmkdkmkefmkkvt--ssgsgtpssfkgtshvlgsgpspssshpaarssn      48
                 |||:|||:.|:|||   ||.|.:.||||||:|||||||.|||     |.||
SEQ_ID_NO_7    1 MMKEKMKDLMRKVTSSSSSSSSSSSSFKGTAHVLGSGPDPSS-----RPSN      45

SEQ_ID_NO_4   49 pspnlrpapkrtspptpptlttdltsftplvcyssrr--pdangtaCava      96
                 |:|:...||:|.:..:....:....::||:..||||  |.|...|....
SEQ_ID_NO_7   46 PTPSRPAAPRREAAASARPPSSGFAPYSPLISTSSRRTDPPAGAGAGEDD      95

SEQ_ID_NO_4   97 tvacpscgdafpselavsehldgclasaggararaaaylaadppppaasv     146
                 .||||||.:.||||||||:|||||||:|||||.||||||.|   |||::|
SEQ_ID_NO_7   96 AVACPSCAEPFPSELAVSDHLDGCLAAAGGARPRAAAYLAGD--PPASAV     143

SEQ_ID_NO_4  147 evvkrllgnllrepgndkfrrvrlgnprikealadrdggvelleavgftv     196
                 |||||||||||.:|.|||:|:|||||||||||||||||||:|||:||||||.|
SEQ_ID_NO_7  144 EVVKRLLGNLLSDPRNDKYRKVRLGNPRIKEALADREGGVDLLEAVGFRV     193

SEQ_ID_NO_4  197 gdeggepfavmdevpsdprlngirravllllegahpsappvkaeaeakesc     246
                 .|||||.||:|||||.|.||.|||:||||||.|.||.|| :.:|:|||:|
SEQ_ID_NO_7  194 ADEGGELFALMDEVPGDARLGGIRQAVLLLERARPSTPP-QTQADAKETC     242

SEQ_ID_NO_4  247 sn-vsdvqegaktidrqirvfvsvpgssmaqndvpdsfyklsgeeirnea     295
                 .|  ||:.|...|.:||||||.||..||:|:||:|||||.||.||||||
SEQ_ID_NO_7  243 PNGVSEEQGIKKPVDRQIRVFFSVAASSVAENDLPDSFYSLSNEEIRNEA     292

SEQ_ID_NO_4  296 kmrrerleqsrllipksykekqalaarqkykqavirvqfpdrmilqgifl     345
                 |||||||||||||||||||||||||||||||||||||||:||:||||.:||||:||
SEQ_ID_NO_7  293 KMRRERLEQSRLLIPKSYKEKQALAARQKYKQALIRIQFPDGVILQGVFL     342

SEQ_ID_NO_4  346 pgeatsslyefvtsalkqsglefelispaipkprvvphfpnpgerartlq     395
                 |.|..|||||||.|:|||..|||:||.||.|:.||:|.||.|||:||||:
SEQ_ID_NO_7  343 PAEPISSLYEFVASSLKQPSLEFDLICPAGPRTRVIPPFPKPGEQARTLR     392

SEQ_ID_NO_4  396 eeelvpsallkfipketdsmvftglldellmaseplpaasq     436
                 :|:||||.|.|.|||||||:||||||||||||...|||..:||.
SEQ_ID_NO_7  393 DEDLVPSARLTFKPKETDSVVFTGLLDELLETSEPFTSASS     433
```
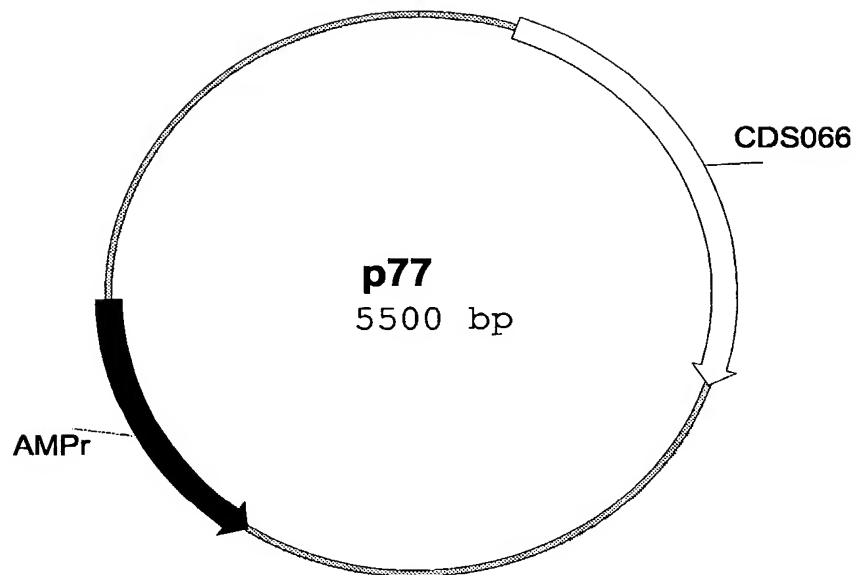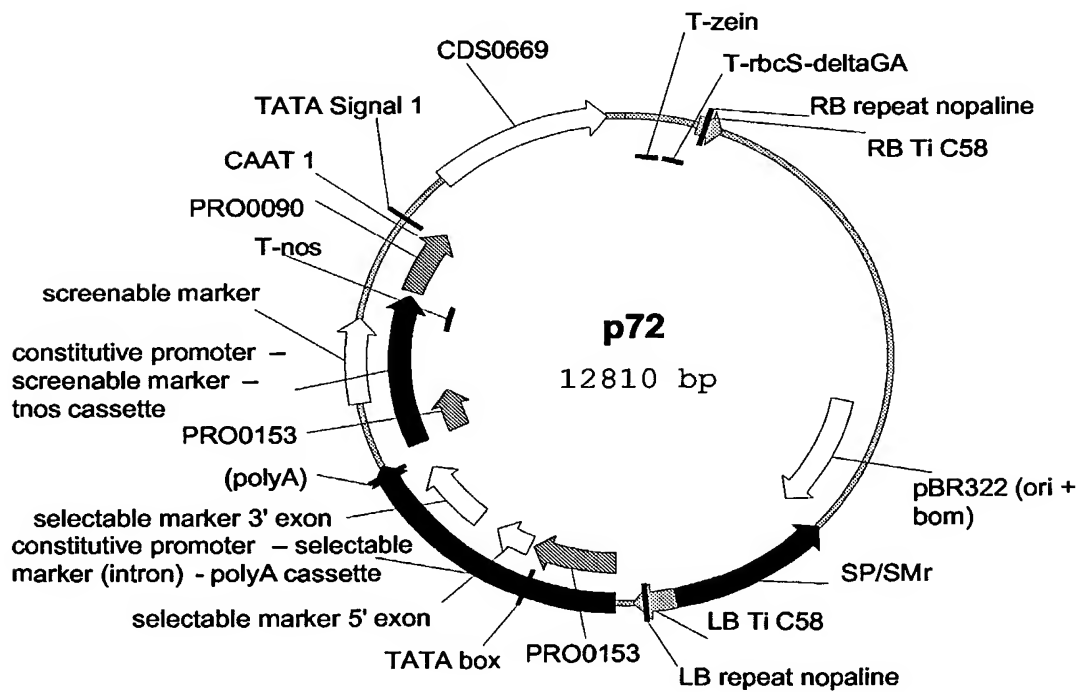
FIGURE 2 E

FIGURE 3

FIGURE 4

SEQ ID NO 1: GRUBX coding sequence
atgggtgacatgaaggataaagtcaaagggttcatgaaaaaagtcacatcttcttcttcaggtaagtttа
aaggccaaggtagggttttgggtggttcatcttcttcaggaccctcaaatcatgtcaataattttttcatc
acatcccctaaatacaaggcaagatcaacaaccttcatatacaaaaacttcgcctcaaaaaccaagtaat
tctgatcaaagaattgagaatatatgtgaaattcagttcaacaaaagtgaatcaaaggatggttttgatc
catttggtgaattagtcacttctgggaagagaaacccaaaagggtattcacttactaatgtgtttgaatg
ccctgtctgtggtagtggttttgtttctgaagaagaggtgtcaactcatattgatagctgtttaagttct
gaagtgtcttctaatttggggagttgaaagtaaagttgaagttaaaagtgaattggaaacatgtgttagtg
catatgtttcagggaagccctcagaagggtcagttgaagtggtcattaagttgttaaagaatattgtgaa
ggaaccagagaatgccaagtttaggaaaataaggatggggaatccaaaaataaaaggtgctataggtgat
gttgtaggaggagtggagctattggaatttgttggatttgagttgaaagaagaaggtggggaaatttggg
ctgtgatggatgttccttctgaagaacaacttgttatgcttaagaatgtagtttcactcttggaaccgaa
gaaggttgaagagttggcgtccttatcccaagttaaggcgagtgaaccagttgagccgaagaagattgat
agacagattcgagtgttctttttctgttcccgagagcgtagcagcaaaaattgagctacctgattccttct
ttaacctctcacgtgaggaattgagaagagaagcagagatgaggaagaagaaattagaagattccaaatt
attgattcctaaatcttatcgggaaaagcaggcaaaagctgcaagaaagaagtacacaaatccattatc
cgtgtacagtttccagatggagcattgcttcaaggtgtctttctaccttcggagccaactagtgctcttt
atgagtttgtgagcgcagcgttaaaggaaccaagcttagagttcgaattgttacatccggtgcttgttaa
aaagcgggtgattccccatttttccagctgctggggagagggctgtaacagttgaagaggaggatttggtt
cctgcagctctactcaaatttaaacctatcgaaacagattctgttgtttttactggtctttgtaatgagc
ttcttgaaattagcgagcccctcgagaccggatcagttgcttcctcgtaa

SEQ ID NO 2: GRUBX, deduced protein sequence
MGDMKDKVKGFMKKVTSSSSGKFKGQGRVLGGSSSSGPSNHVNNFSSHPLNTRQDQQPSYTKTSPQKPSN
SDQRIENICEIQFNKSESKDGFDPFGELVTSGKRNPKGYSLTNVFECPVCGSGFVSEEEVSTHIDSCLSS
EVSSNLGVESKVEVKSELETCVSAYVSGKPSEGSVEVVIKLLKNIVKEPENAKFRKIRMGNPKIKGAIGD
VVGGVELLEFVGFELKEEGGEIWAVMDVPSEEQLVMLKNVVSLLEPKKVEELASLSQVKASEPVEPKKID
RQIRVFFSVPESVAAKIELPDSFFNLSREELRREAEMRKKKLEDSKLLIPKSYREKQAKAARKKYTKSII
RVQFPDGALLQGVFLPSEPTSALYEFVSAALKEPSLEFELLHPVLVKKRVIPHFPAAGERAVTVEEEDLV
PAALLKFKPIETDSVVFTGLCNELLEISEPLETGSVASS

SEQ ID NO 3: *GRUBX* orthologue from sugarcane
atgatgaaggacaagatgaaggagttcatgaagaaggtcacctcctccgggtccgggacccctcctcct
tcaagggcacctcccacgtcctcggctccggcccctcccccctcctcctcccacccgctgcccgctcctc
aaaccctagcccaaacctcaggcccgctcctaagcggacctcgccacctaccccgcccactttaaccacc
gatttgacctccttcacgcccctcgtctgctactcctcccgccgccccgacgcgaacggcaccgcgnnng
ccgtcgccaccgtcgcgtgccccagctgcggagacgcgtttcgtccgagctcgccgtctccgagcatct
cgacggctgcctcgcgtcggcggggggcgcccgcgcgcgcgccgccgcgtacctcgccgccgacccgcct
ccgcccgcggcctccgtagaggtggtcaaacgcctgctgggcaacctgctccgggagcccggcaacgata
agttcaggcgggtgagattgggtaacccgcggatcaaggaggccctggcagacagggatggcggggtgga
gctcctggaggccgtcggcttcacagttggggatgagggcggggagcccttcgccgtgatggacgaagtg
cctagcgaccctaggctcaacgggatcaggagggccgtcctcctgctcgagggggcacacccctctgcgc
ctccagtgaaggcggaggctgaggccaaggagagctgcagcaatgtgtctgacgtgcaggagggtgctaa
gactattgatcggcagattcgggtatttgtctctgttcctgggagttctatggcacaaaatgatgtacca
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aatctcgattgctgataccaaagtcttacaaggagaaacaggcattggctgctcgacagaagtataaaca
agcagtcattcgagttcagtttccagatagaatgattcttcagggcatattcctaccaggagaggccact
agttcactgtatgagttcgtcacatctgctctgaagcaatcaggtttggaattcgaacttatctctccag
ccatacctaagccacgtgtggtgccccattttccaaacccgggagagcgggcacgcaccttgcaagagga
ggagctggtcccatctgcgctcctcaagttcattcccaaggagactgattccatggttttcaccggtttg
cttgatgagcttctcatggccagtgagccgcttcctgctgcatcacaatga

FIGURE 5

SEQ ID NO 4: sugarcane GRUBX orthologue, deduced protein sequence
MMKDKMKEFMKKVTSSGSGTPSSFKGTSHVLGSGPSPSSSHPAARSSNPSPNLRPAPKRTSPPTPPTLTT
DLTSFTPLVCYSSRRPDANGTAXAVATVACPSCGDAFPSELAVSEHLDGCLASAGGARARAAAYLAADPP
PPAASVEVVKRLLGNLLREPGNDKFRRVRLGNPRIKEALADRDGGVELLEAVGFTVGDEGGEPFAVMDEV
PSDPRLNGIRRAVLLLEGAHPSAPPVKAEAEAKESCSNVSDVQEGAKTIDRQIRVFVSVPGSSMAQNDVP
DSFYKLSGEEIRNEAKMRRERLEQSRLLIPKSYKEKQALAARQKYKQAVIRVQFPDRMILQGIFLPGEAT
SSLYEFVTSALKQSGLEFELISPAIPKPRVVPHFPNPGERARTLQEEELVPSALLKFIPKETDSMVFTGL
LDELLMASEPLPAASQ

SEQ ID NO 5: expression cassette comprising *GRUBX* (1011-2390) operably linked to the prolamine promoter (1-654) and the T-Zein + T-Rubisco deltaG terminator (2615-2808 and 2852-3048):
cttctacatcggcttaggtgtagcaacacgactttattattattattattattattattattttaca
aaaatataaaatagatcagtccctcaccacaagtagagcaagttggtgagttattgtaaagttctacaaa
gctaatttaaaagttattgcattaacttatttcatattacaaacaagagtgtcaatggaacaatgaaaac
catatgacatactataattttgttttтattattgaaattatataattcaaagagaataaatccacatagc
cgtaaagttctacatgtggtgcattaccaaaatatatatagcttacaaaacatgacaagcttagtttgaa
aaattgcaatccttatcacattgacacataaagtgagtgatgagtcataatattattttctttgctaccc
atcatgtatatatgatagccacaaagttactttgatgatgatatcaaagaacatttttaggtgcacctaa
cagaatatccaaataatatgactcacttagatcataatagagcatcaagtaaaactaacactctaaagca
accgatgggaaagcatctataaatagacaagcacaatgaaaatcctcatcatccttcaccacaattcaaa
tattatagttgaagcatagtagtaatttaaatcaactagggatatcacaagtttgtacaaaaaagcaggc
tggtaccggtccggaattcccgggatatcgtcgacccacgcgtccgccaatatcagatttctttcatgaa
ctccacttccaatttctcattgcttcttcttcccatttccacctccaaagccatccttccagaaaacctt
gttccttacatttcttagccccaaaaaagattcccatctcaattccacaaaaaaacacaaggagatctaa
ggaaattccccgcctctatatatagagaggtggaattgttcctgaatttggtttgaattgattgattgac
agattttggtgagagggtgttattgaaaaa**atg**ggtgacatgaaggataaagtcaaagggttcatgaaaa
aagtcacatcttcttcttcaggtaagtttaaaggccaaggtagggttttgggtggttcatcttcttcagg
accctcaaatcatgtcaataatttttcatcacatcccctaaatacaaggcaagatcaacaaccttcatat
acaaaaacttcgcctcaaaaaccaagtaattctgatcaaagaattgagaatatatgtgaaattcagttca
acaaaagtgaatcaaaggatggttttgatccatttggtgaattagtcacttctgggaagagaaacccaaa
agggtattcacttactaatgtgtttgaatgccctgtctgtggtagtggttttgtttctgaagaagaggtg
tcaactcatattgatagctgtttaagttctgaagtgtcttctaatttgggagttgaaagtaaagttgaag
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aatccaaaaataaaaggtgctataggtgatgttgtaggaggagtggagctattggaatttgttggatttg
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taagaatgtagtttcactcttggaaccgaagaaggttgaagagttggcgtccttatcccaagttaaggcg
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gaggaagaagaaattagaagattccaaattattgattcctaaatcttatcgggaaaagcaggcaaaagct
gcaagaaagaagtacacaaatccattatccgtgtacagtttccagatggagcattgcttcaaggtgtct
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gttcgaattgttacatccggtgcttgttaaaaagcgggtgattccccattttccagctgctggggagagg
gctgtaacagttgaagaggaggatttggttcctgcagctctactcaaatttaaacctatcgaaacagatt
ctgttgttttttactggtctttgtaatgagcttcttgaaattagcgagcccctcgagaccggatcagttgc
ttcctcg**taa**gctctaaattacatcagactttgaattcttctgagtgttggaaaccttataaaactctct
gcgccgggaatgctgcggccgctctagagtatccctcgaggggcccaagcttacgcgtacccagctttct
tgtacaaagtggtgatatcacaagcccgggcggtcttctagggataacagggtaattatatccctctaga
tcacaagcccgggcggtcttctacgatgattgagtaataatgtgtcacgcatcaccatgggtggcagtgt

FIGURE 5 (continued)

cagtgtgagcaatgacctgaatgaacaattgaaatgaaaagaaaaaagtactccatctgttccaaatta
aaattcatttttaaccttttaataggtttatacaataattgatatatgttttctgtatatgtctaatttgt
tatcatccgggcggtcttctagggataacagggtaattatatccctctagacaacacacaacaaataaga
gaaaaaacaaataatattaatttgagaatgaacaaaaggaccatatcattcattaactcttctccatcca
tttccatttcacagttcgatagcgaaaaccgaataaaaaacacagtaaattacaagcacaacaaatggta
caagaaaaacagttttcccaatgccataatactcgaac

SEQ ID NO 6: *Oryza sativa GRUBX* **orthologue, DNA sequence**
atgatgaaggaaaagatgaaggatctcatgaggaaggtcacctcctcctcctcctcctcgtcgtcct
cctccttcaagggcaccgcccacgtcctcggctccggccccgacccctcctcccgcccctccaaccctac
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SEQ ID NO 7: *Oryza sativa GRUBX* **orthologue, deduced protein sequence**
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LLETSEPFTSASS

FIGURE 5 (continued)